



01 13 06 SeqListg CEN0250NP.txt

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<120> ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES

<130> CEN0250 NP

<140> US 09/920,137

<141> 2001-08-01

<150> 60/223,360

<151> 2000-08-07

<150> 60/236,826

<151> 2000-09-29

<160> 35

<170> PatentIn Ver 3.1

<210> 1

<211> 5

<212> PRT

<213> Homo sapiens

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<222> (1)..(5)

<223> Heavy Chain complementarity determinng region 1 (CDR1).

<400> 1

Ser Tyr Ala Met His
1 5

<210> 2

<211> 17

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<222> (1)..(17)

<223> Heavy Chain complementarity determinng region 2 (CDR2).

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<222> (1)..(1)

<223> xaa at position 1 is selected from Ile, Phe or Val.

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> xaa at position 2 is selected from Ile or Met.

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa at position 3 is selected from Ser or Leu.

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa at position 4 is selected from Tyr or Phe.

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa at position 10 is selected from Lys or Tyr.

<220>

<221> MISC_FEATURE

<222> (11)..(11)

<223> Xaa at position 11 is selected from Ser or Tyr.

<220>

<221> MISC_FEATURE

<222> (17)..(17)

<223> Xaa at position 17 is selected from Asp or Gly.

<400> 2

	Xaa	Xaa	Xaa	Xaa	Asp	Gly	Ser	Asn	Lys	Xaa	Xaa	Ala	Asp	Ser	Val	Lys	Xaa
1					5				10					15			

<210> 3

<211> 17

<212> PRT

<213> Homo sapiens

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<222> (1)..(17)

<223> Heavy Chain complementarity determining region 3 (CDR3).

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa at position 4 is selected from Ile or Val.

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Xaa at position 5 is selected from Ser, Ala or Gly.

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> Xaa at position 9 is selected from Asn or Tyr.

<400> 3

	Asp	Arg	Gly	Xaa	Xaa	Ala	Gly	Gly	Xaa	Tyr	Tyr	Tyr	Tyr	Gly	Met	Asp	Val
1					5				10					15			

<210> 4

<211> 11

<212> PRT

<213> Homo sapiens

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<220>
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 <222> (1)..(11)
 <223> Light Chain complementarity determinng region 1 (CDR1).

<220>
 <221> MISC_FEATURE
 <222> (7)..(7)
 <223> Xaa at position 7 is selected from Ser or Tyr.

<400> 4
 Arg Ala Ser Gln Ser Val Xaa Ser Tyr Leu Ala
 1 5 10

<210> 5
 <211> 7
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(7)
 <223> Light chain complementarity determinng region 2 (CDR2).

<400> 5
 Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 6
 <211> 10
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (1)..(10)
 <223> Light chain complementarity determinng region 3 (CDR3).

<400> 6
 Gln Gln Arg Ser Asn Trp Pro Pro Phe Thr
 1 5 10

<210> 7
 <211> 126
 <212> PRT
 <213> Homo sapiens
 <400> 7

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu Trp Val
 35 40 45

Ala Phe Met Ser Tyr Asp Gly Ser Asn Lys Lys Tyr Ala Asp Ser Val
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50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Arg Gly Ile Ala Ala Gly Gly Asn Tyr Tyr Tyr Tyr Gly
 100 105 110
 Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 8
 <211> 108
 <212> PRT
 <213> Homo sapiens
 <400> 8

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr Ser Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
 85 90 95
 Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 9
 <211> 157
 <212> PRT
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<220>
 <221> MISC_FEATURE
 <222> (1)..(157)
 <223> human TNF alpha monomer sequence

<400> 9

Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
 1 5 10 15
 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
 20 25 30
 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
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35

40

45

Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
 50 55 60
 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
 65 70 75 80
 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
 85 90 95
 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
 100 105 110
 Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
 115 120 125
 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
 130 135 140
 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
 145 150 155

<210> 10
 <211> 18
 <212> DNA
 <213> Homo sapiens

<400> 10

ttgggtccagt cggactgg

18

<210> 11
 <211> 18
 <212> DNA
 <213> Homo sapiens

<400> 11

cacctgcact cgggtgctt

18

<210> 12
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 12

cactgttttg agtgtgtacg ggcttaagtt

30

<210> 13
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<400> 13

gccgcacgtg tggaaggg

18

<210> 14
 <211> 25
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<400> 14
 agtcaagggtc ggactggctt aagtt 25

<210> 15
 <211> 28
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<400> 15
 gttgtcccct ctcacaatct tcgaattt 28

<210> 16
 <211> 18
 <212> DNA
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<400> 16
 ggcggtagac tactcgtc 18

<210> 17
 <211> 7
 <212> PRT
 <213> Homo sapiens

<400> 17
 Met Asp Trp Thr Trp Ser Ile
 1 5

<210> 18
 <211> 35
 <212> DNA
 <213> Homo sapiens

<400> 18
 tttcgtacgc caccatggac tggacctgga gcatc 35

<210> 19
 <211> 34
 <212> DNA
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<400> 19
 tttcgtacgc caccatgggg tttgggctga gctg 34

<210> 20
 <211> 35
 <212> DNA
 <213> Homo sapiens

<400> 20
 tttcgtacgc caccatggag tttgggctga gcatg 35

<210> 21
 <211> 35

<212> DNA
<213> Homo sapiens

<400> 21

tttcgtacgc caccatgaaa cacctgtggt tcttc 35

<210> 22
<211> 35
<212> DNA
<213> Homo sapiens

<400> 22

tttcgtacgc caccatgggg tcaaccgccca tcctc 35

<210> 23
<211> 6
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<400> 23

Thr Val Thr Val Ser Ser
1 5

<210> 24
<211> 36
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<400> 24

gtgccagtgg cagaggagtc cattcaagct taagtt 36

<210> 25
<211> 5
<212> PRT
<213> Homo sapiens

<400> 25

Met Asp Met Arg Val
1 5

<210> 26
<211> 31
<212> DNA
<213> Homo sapiens

<400> 26

tttgtcgaca ccatggacat gagggctctc c 31

<210> 27
<211> 28
<212> DNA
<213> Homo sapiens

<400> 27

tttgtcgaca ccatggaagc cccagctc 28

<210> 28
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 28

Thr Lys Val Asp Ile Lys
 1 5

<210> 29
 <211> 41
 <212> DNA
 <213> Homo sapiens

<400> 29

ctggtttcac ctatagtttg cattcagaat tcggcgctt t 41

<210> 30
 <211> 35
 <212> DNA
 <213> Homo sapiens

<400> 30

catctccaga gacaattcca agaacacgct gtatc 35

<210> 31
 <211> 35
 <212> DNA
 <213> Homo sapiens

<400> 31

gtagaggtct ctgttaaggt tcttgtgcga catag 35

<210> 32
 <211> 19
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(19)
 <223> Signal sequence for heavy chain variable region sequences as presented in original

Figure 4

<400> 32

Met Gly Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
 1 5 10 15
 Val Gln Cys

<210> 33
 <211> 20
 <212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(20)

<223> Signal sequence for light chain variable region sequences as presented in original

Figure 5

<400> 33

Met	Glu	Ala	Pro	Ala	Gln	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Trp	Leu	Pro
1				5					10					15	
Asp	Thr	Thr	Gly												
				20											

<210> 34

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(421)

<223> heavy chain variable region DNA sequences as presented in original Figure 2A-2B

<400> 34

atgggggttg	ggctgagctg	ggttttcctc	gttgctcttt	taagaggtgt	ccagtgtcag	60
gtgcagctgg	tggagtctgg	gggaggcggtg	gtccagcctg	ggagggtccct	gagactctcc	120
tgtgcagcct	ctgggttcacc	ttcagtagct	atgctatgca	ctgggtccgc	caggctccgg	180
caaggggctg	gagtgggtgg	cagttatata	atatgatgga	aaataaatac	tacgcagact	240
ccgtgaagg	ccgattcacc	atctagagac	aattccaaga	acacgctgta	tctgcaaagt	300
aacagccaga	gctgaggaca	cggctgtgta	ttactgtgcg	agagatcgag	gtatatcagc	360
aggtggaata	ctactactac	tacggtatgg	acgtctgggg	gcaagggacc	acggtcaccg	420
tctcctca						428

<210> 35

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(387)

<223> light chain variable region DNA sequences as presented in original Figure 3

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atggaagccc	cagctcagct	tctcttcctc	ctgtactctt	ggctcccaga	taccaccgga	60
gaaatttgt	tgacacagtc	tccagccacc	ctgtctttgt	ctccagggga	aagagccacc	120
ctctcctgca	gggccagtc	gagtgttagc	agctacttag	cctggtagca	acagaaacct	180
ggccaggctc	ccaggctcct	catctatgat	gcatccaaca	gggccactgg	catcccagcc	240
aggttcagtg	gcagtgggtc	tgggacagac	ttcactctca	ccatcagcag	cctagagcct	300
gaagattttg	cagtttatta	ctgtcagcag	cgtagcaact	ggcctccatt	cactttcggc	360
cctgggacca	aagtggatat	caaacgt				387